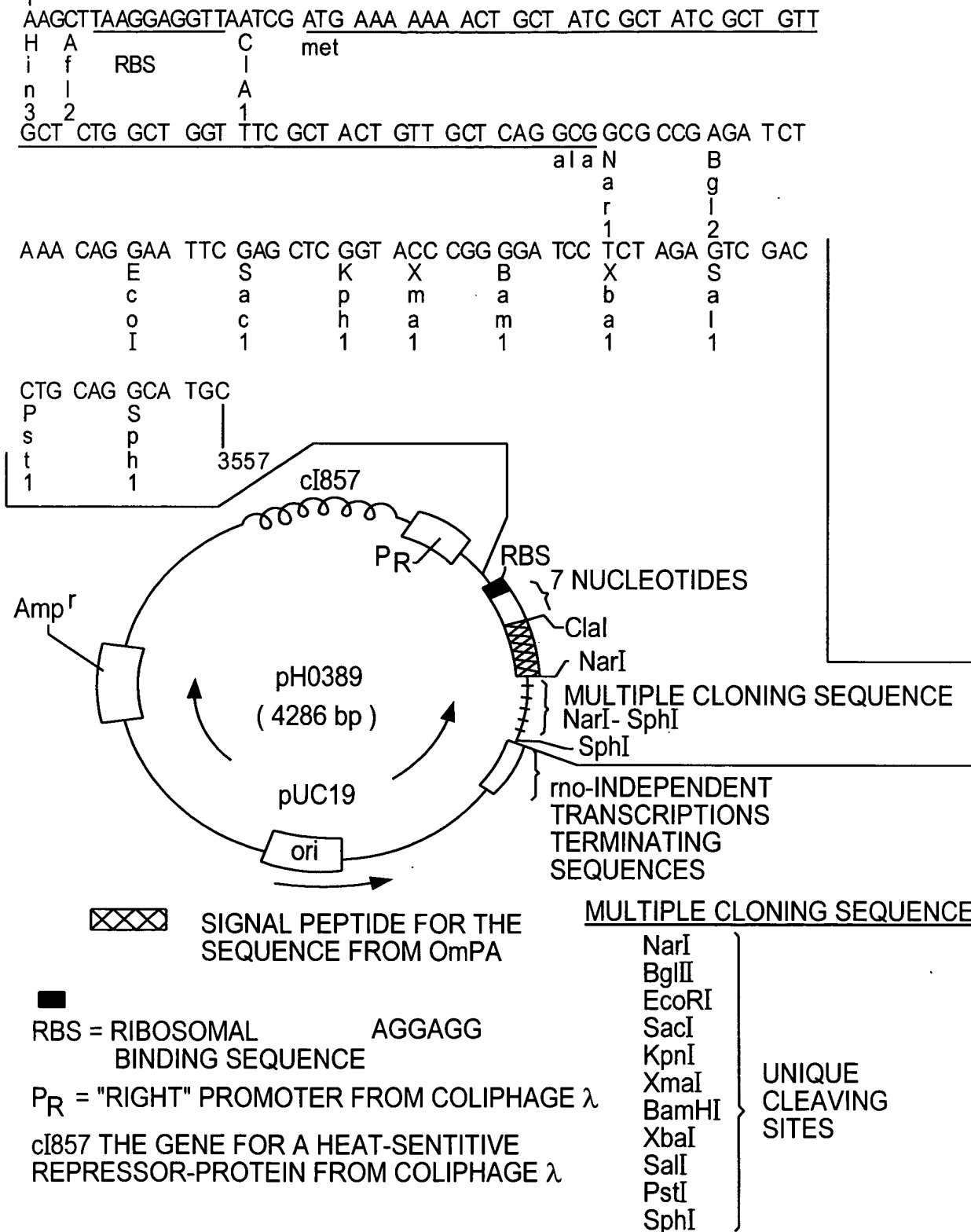




FIG. 1



PLASMA pH0389. THE RIBOSOMAL BINDING-SEQUENCE (EMPHASIZED WITH A FULL LINE), THE SEQUENCE FOR SIGNAL PEPTIDE FROM ompA (FROM E.coli) (DOTTED LINE) AND RECOGNITION SEQUENCE FOR SEVERAL RESTRICTION ENZYMES ARE SHOWN.



2 / 18

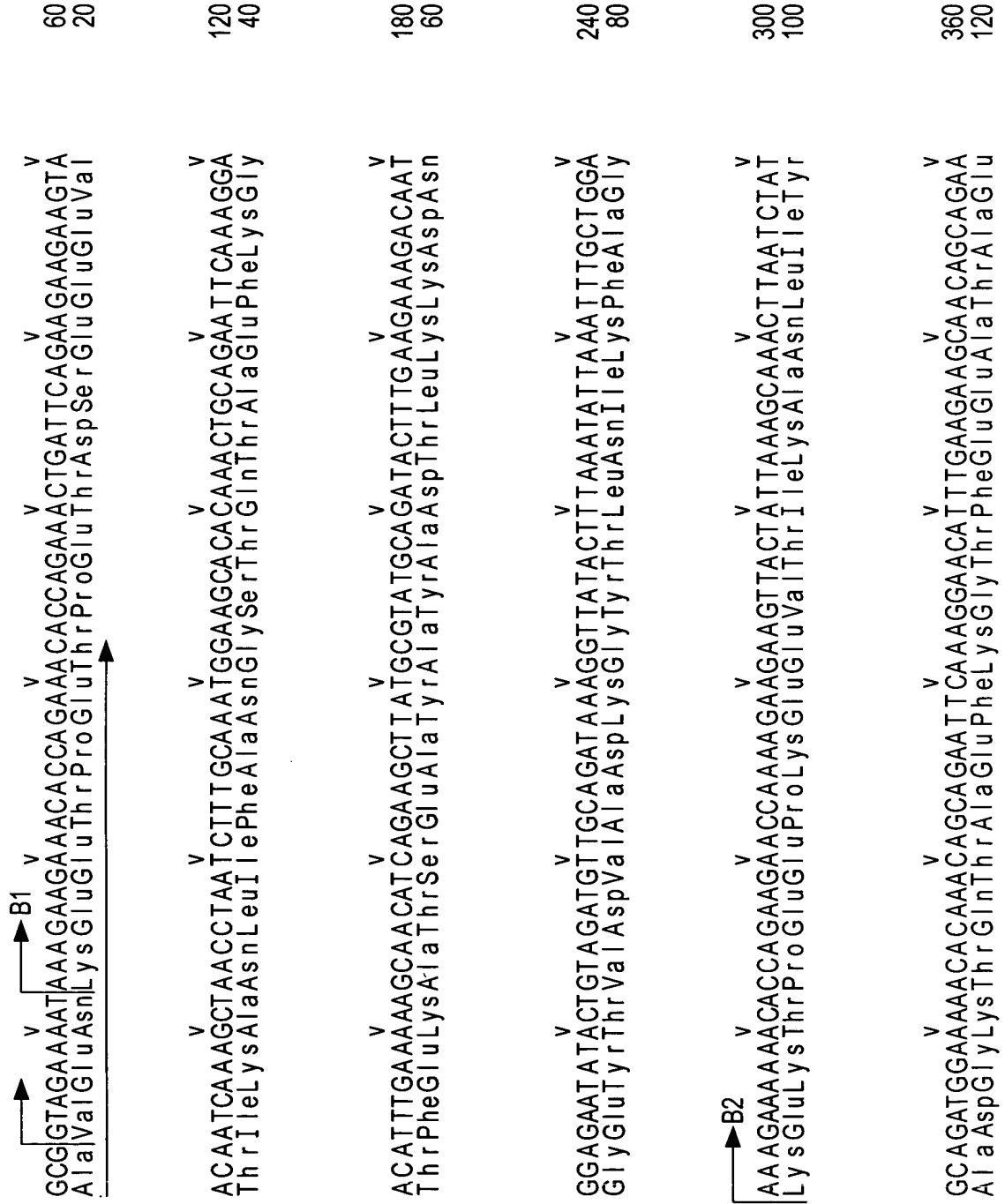


FIG. 2b



GCATACAGATATGCAGATGCATTAAAGAAAGGACAATGGAGAAATATACAGTAGACGTTGCA
AlaTyrArgTyrAlaAspAlaLeuLysLysAspAsnGlyGluTyrThrValAspValAla
420
140

GATAAAGGTTACTTTTAAATATTAAATTTGCTGGAAAGAAAAACACCAGAAAGAACCA
AspLysGlyTyrThrLeuAsnIleLysPheAlaGlyLysGluLysThrProGluGluPro
480
160

AAAGAAGAAGTTACTATTAAAGCAAACTTAATCTATGCAGATGGAAAAACACAAACAGCA
LysGluGluValThrIleLysAlaAsnLeuIleTyrAlaAspGlyLysThrGlnThrAla
540
180

GAATTCAAAGGAACATTTGAAGAAGCAACAGCAGAAAGCATACAGATATGCTGACTTATTA
GluPheLysGlyThrPheGluGluAlaThrAlaGluAlaTyrArgTyrAlaAspLeuLeu
600
200

GCAAAAGAAAATGGTAAATATACAGTAGACGTTGCAGATAAAGGTTATACTTTAAATATT
AlaLysGluAsnGlyLysTyrThrValAspValAlaAspLysGlyTyrThrLeuAsnIle
660
220

AAATTTGCTGGAAGAAAAAACACCCAGAAAGAACCAAGAAAGTTACTATTAAAGCA
LysPheAlaGlyLysGluLysThrProGluGluProLysGluGluValThrIleLysAla
720
240

AACTTAATCTATGCAGATGGAAAAACTCAAACAGCAGAGTTCAAAGGAACATTTGCAGAA
AsnLeuIleTyrAlaAspGlyLysThrGlnThrAlaGluPheLysGlyThrPheAlaGlu
780
260

FIG. 2c

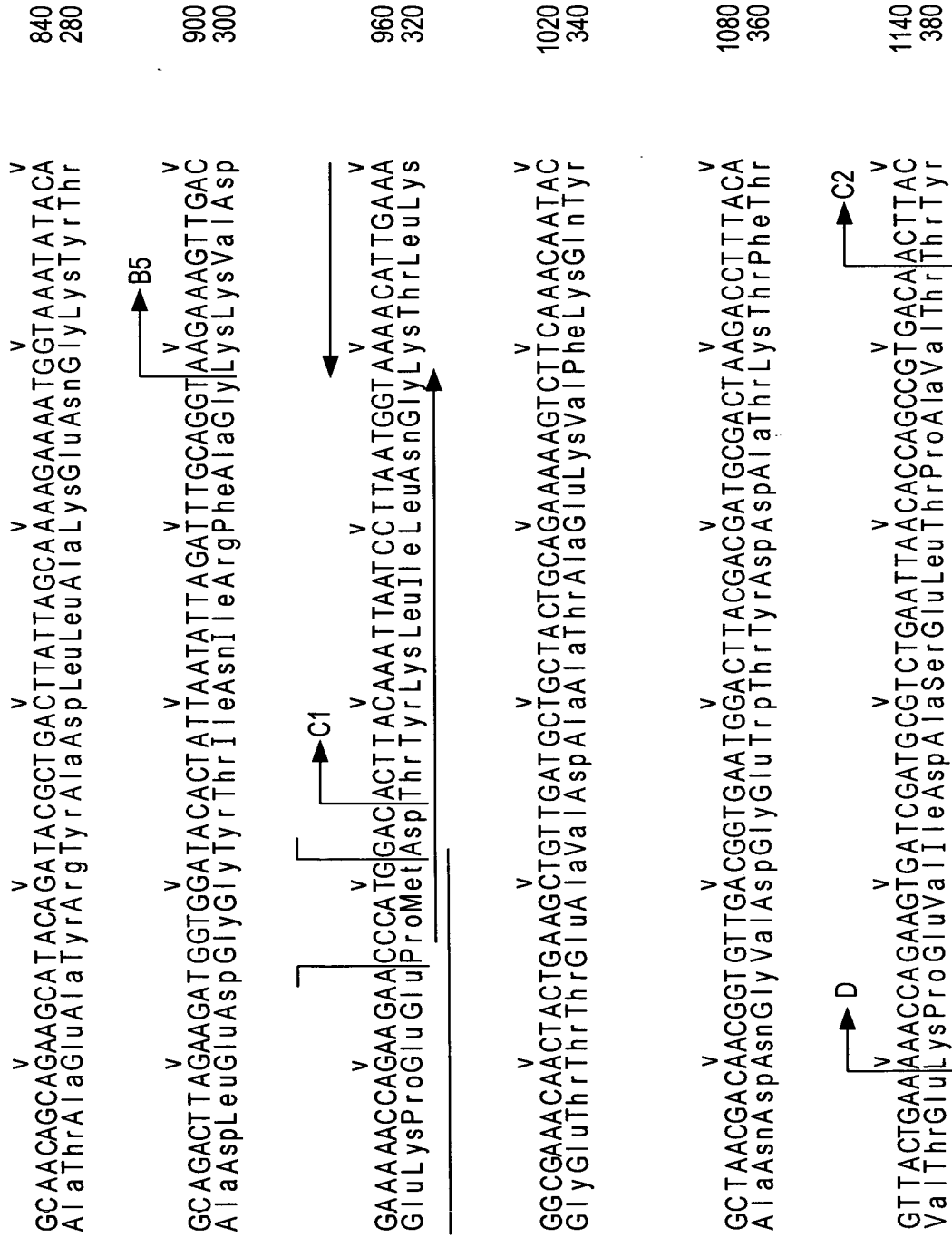


FIG. 2d



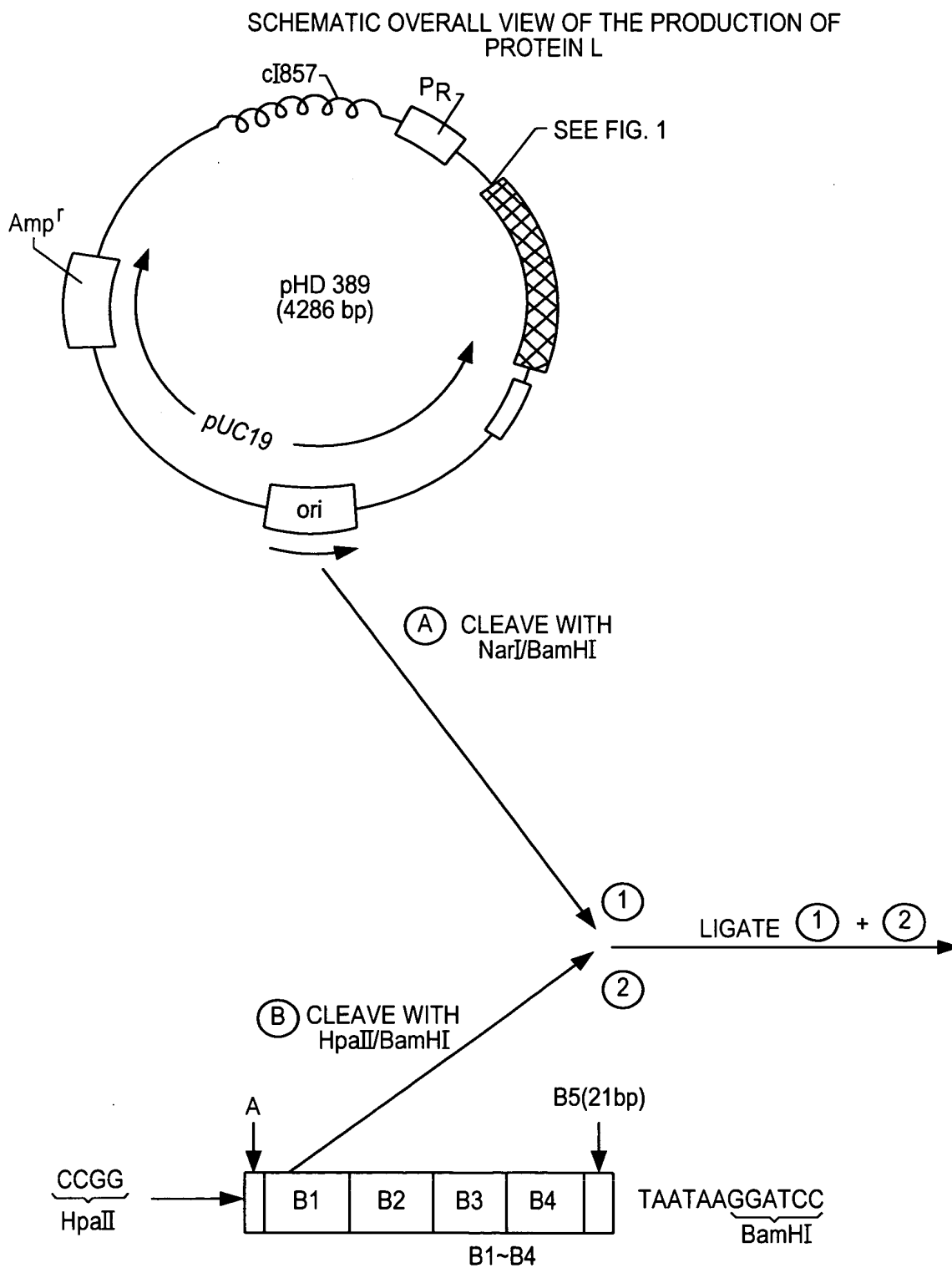
V AAACTTGTATTAAATGGTAAACACATTGAAAGCGGAAACAACTACTAAAGCAGTAGACGCA LysLeuValIleAsnGlyLysThrLeuLysGlyGluThrThrThrLysAlaValAspAla	1200 400
V GAAACTGCAGAAAAAGCCTTCAAACAATACGCTAACGACACACGGTGTGATGGTGTGTTGG GluThrAlaGluLysAlaPheLysGlnTyrAlaAsnAspAsnGlyValAspGlyValTrp	1260 420
V ACTTATGATGATGCGACTAAGACCTTTACGGTAACTGAAATGTGTAATAA ThrTyrAspAspAlaThrLysThrPheThrValThrGluMet - -	1308 434

FIG. 2e



6 / 18

FIG. 3(1)



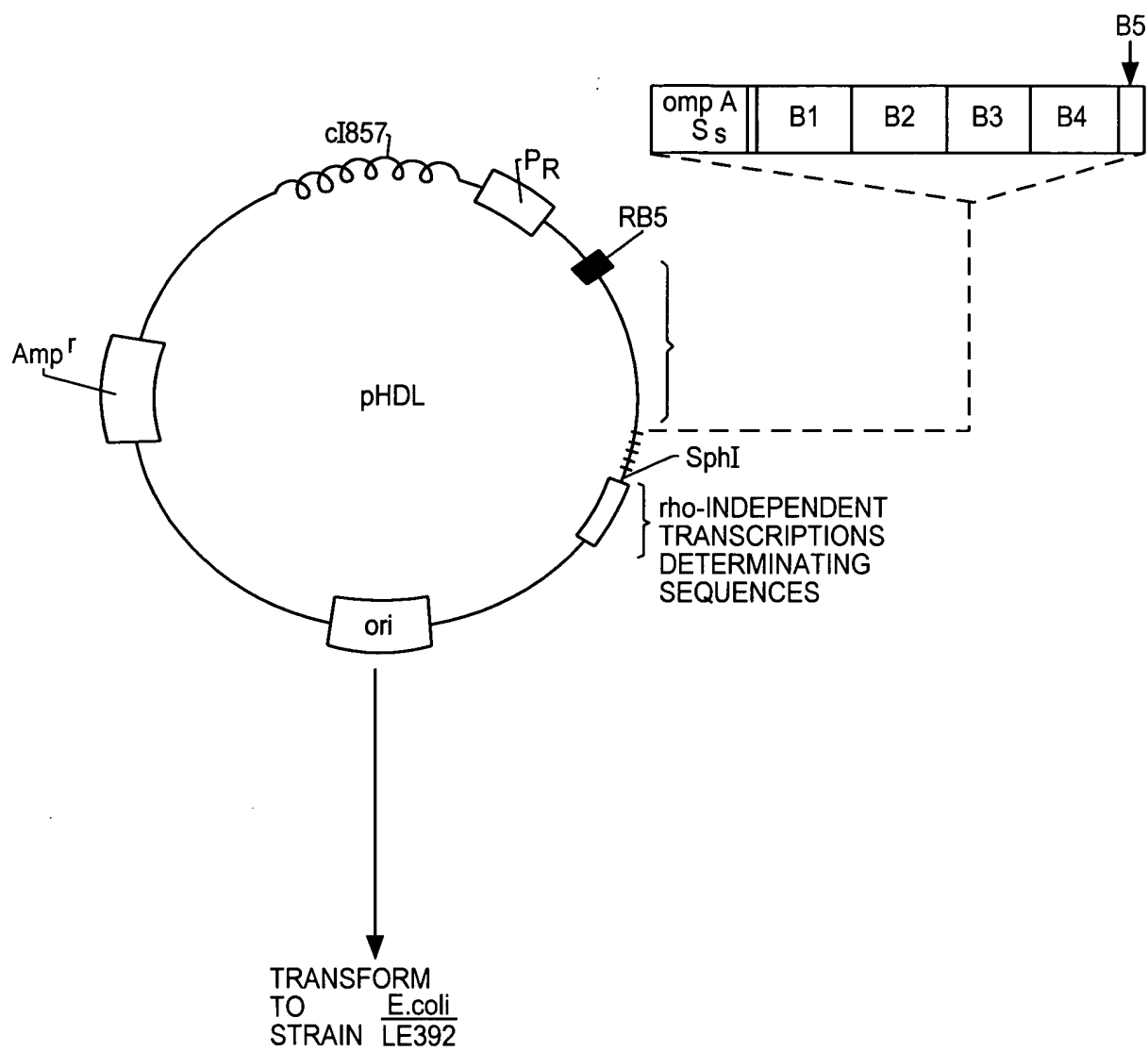


FIG. 3(2)

SCHEMATIC OVERALL VIEW OF PRODUCTION OF PROTEIN LG

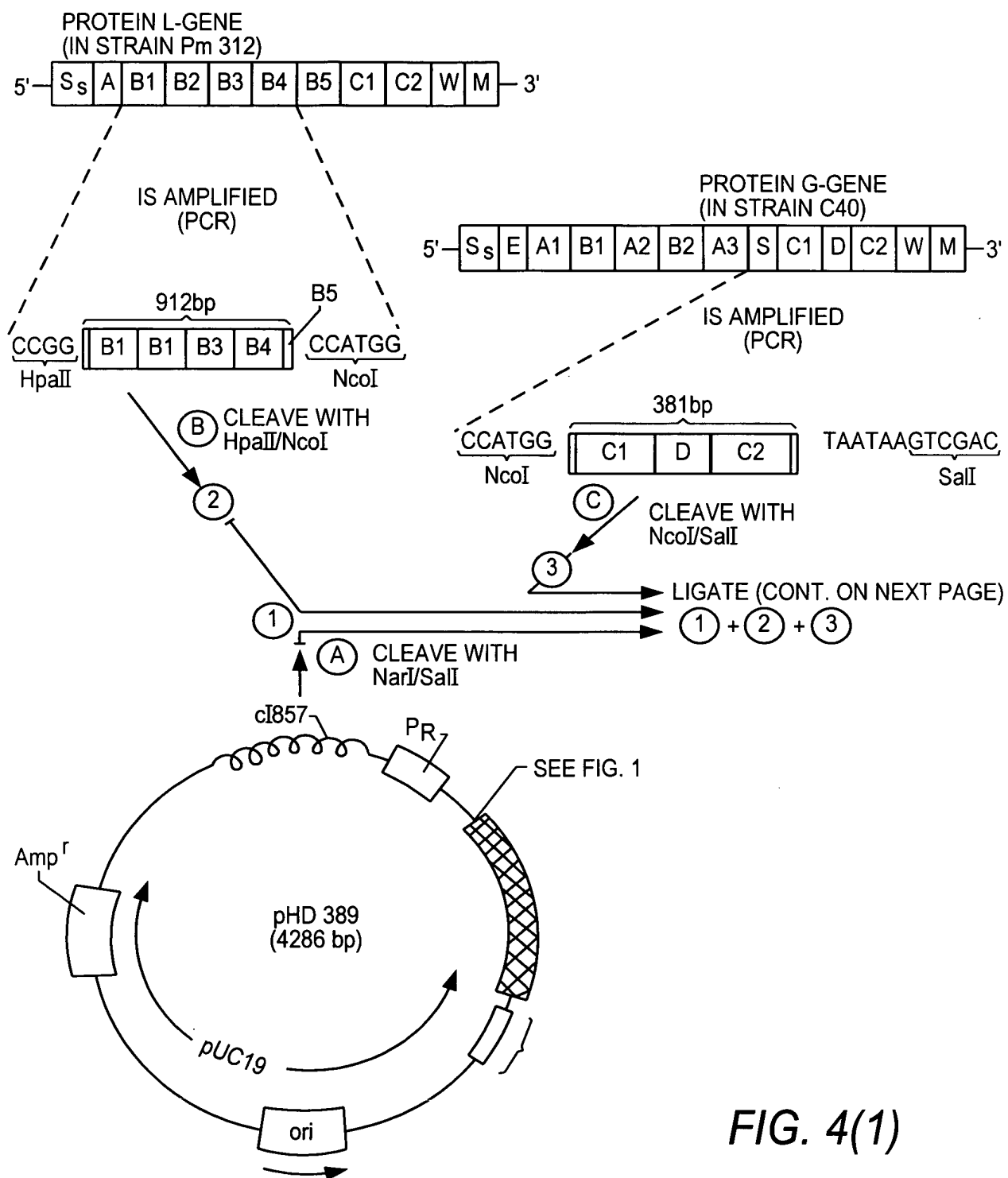


FIG. 4(1)



9 / 18

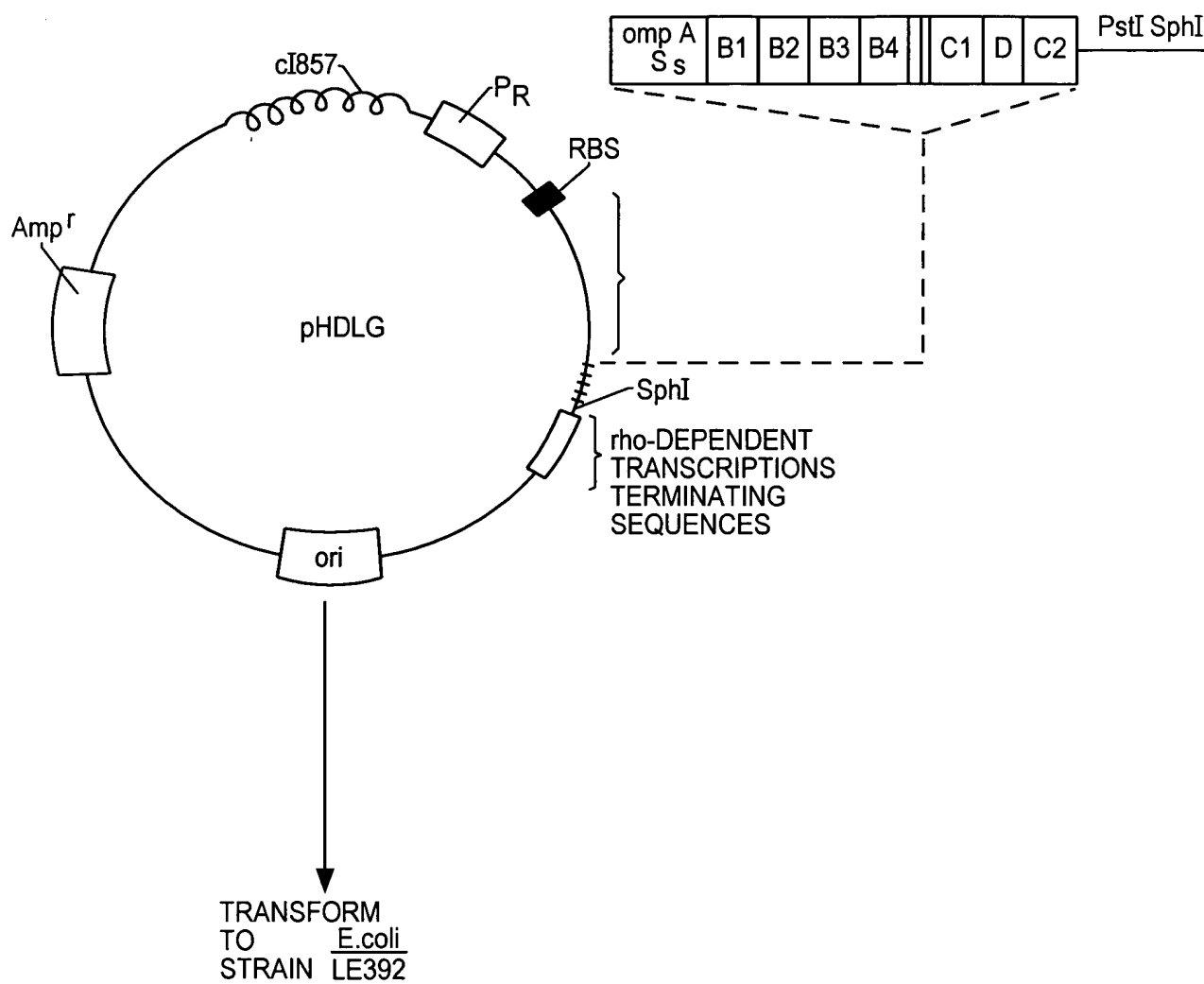


FIG. 4(2)



10 / 18

SCHEMATIC OVERALL VIEW OF PRODUCTION OF PROTEIN LA

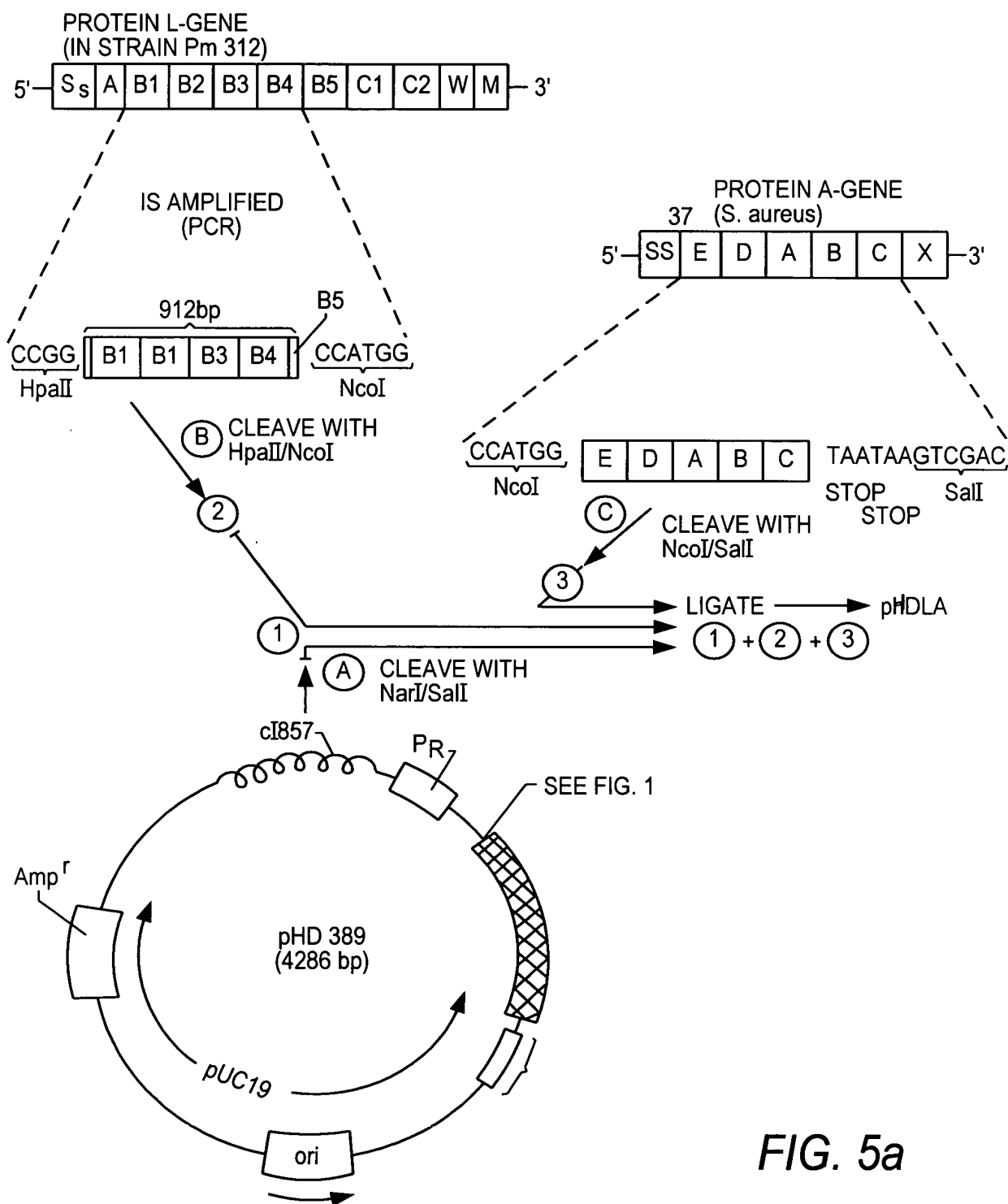


FIG. 5a

SCHEMATIC OVERALL VIEW OF PRODUCTION OF PROTEIN LM

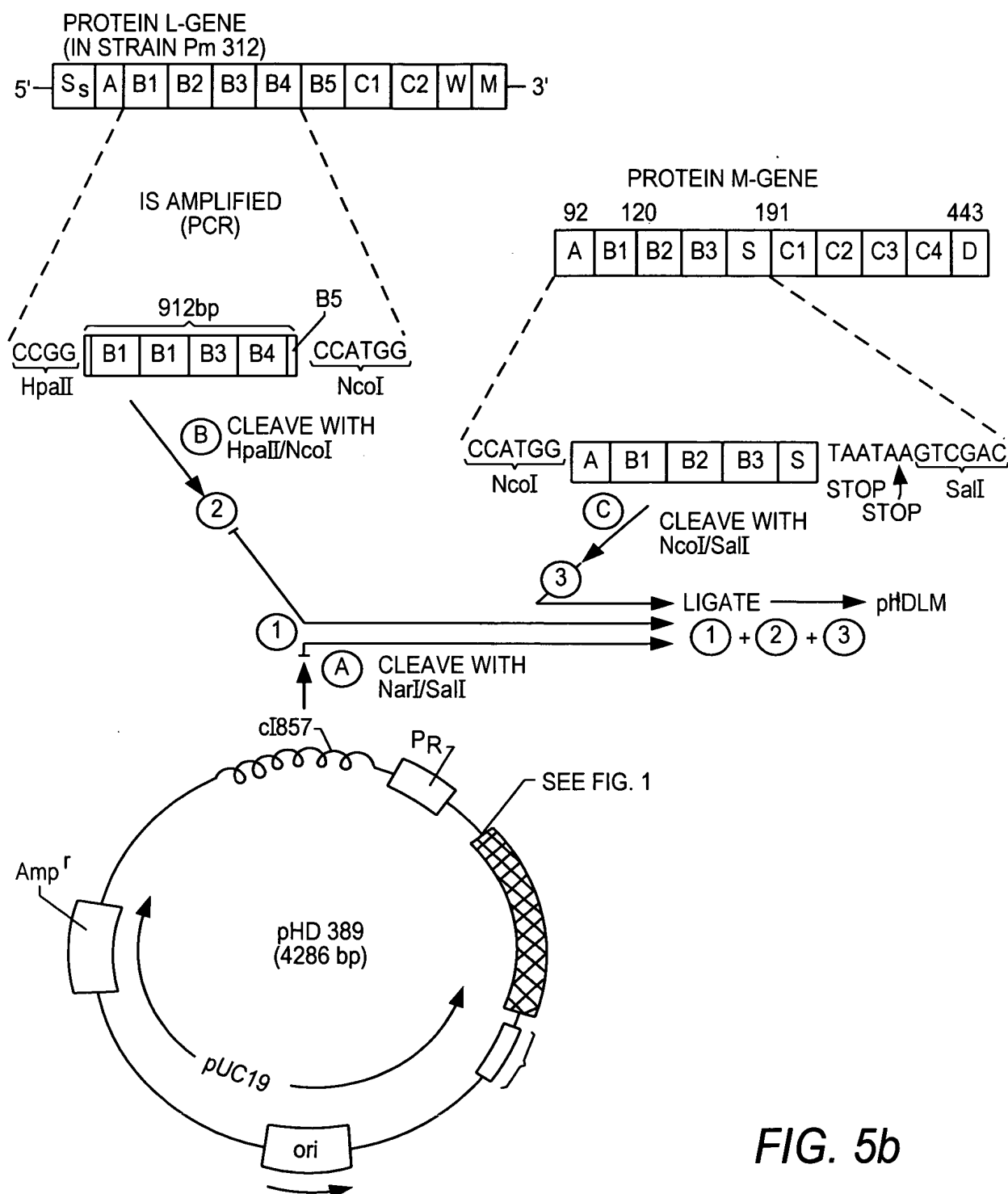


FIG. 5b

SCHEMATIC OVERALL VIEW OF PRODUCTION OF PROTEIN LH

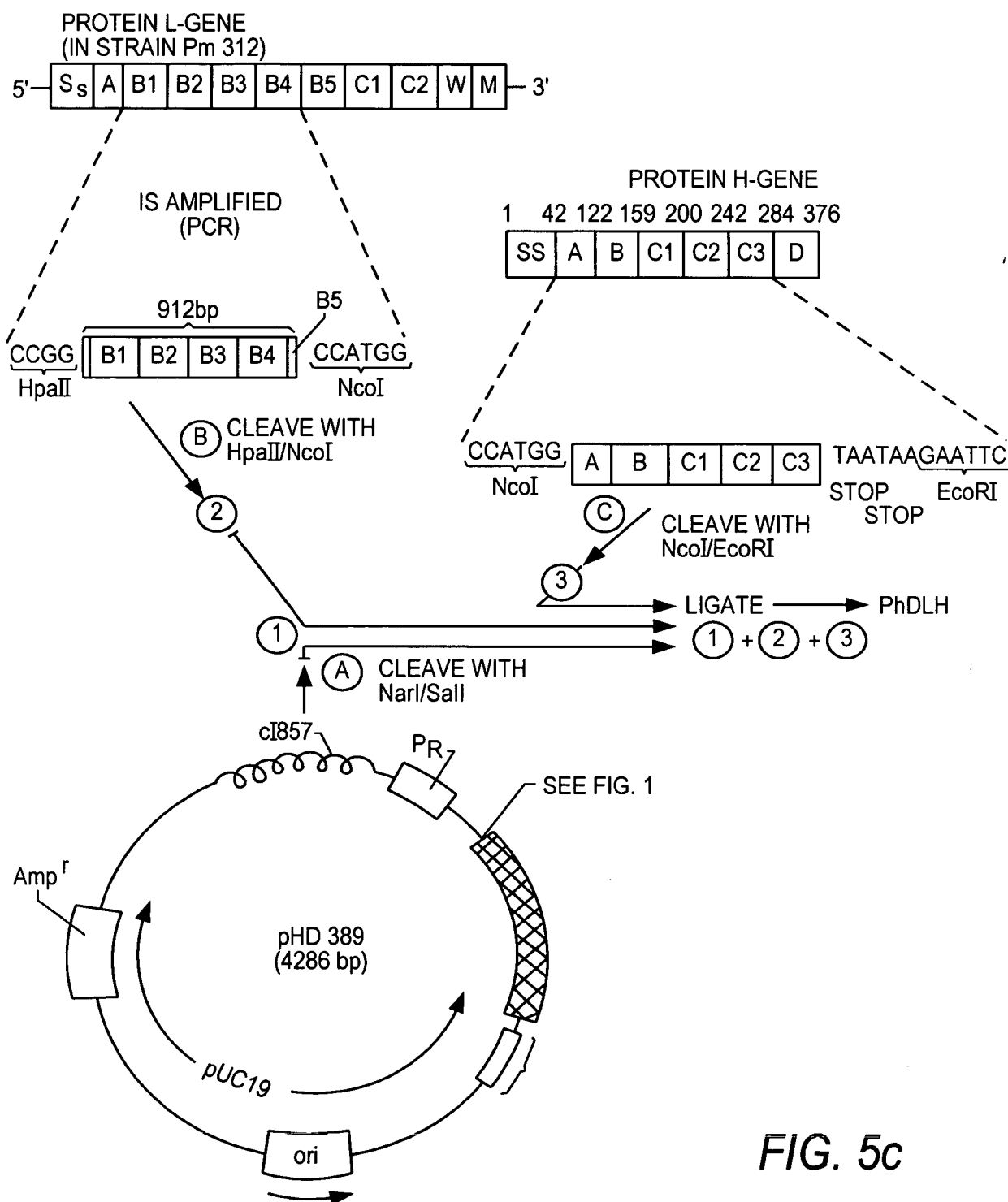
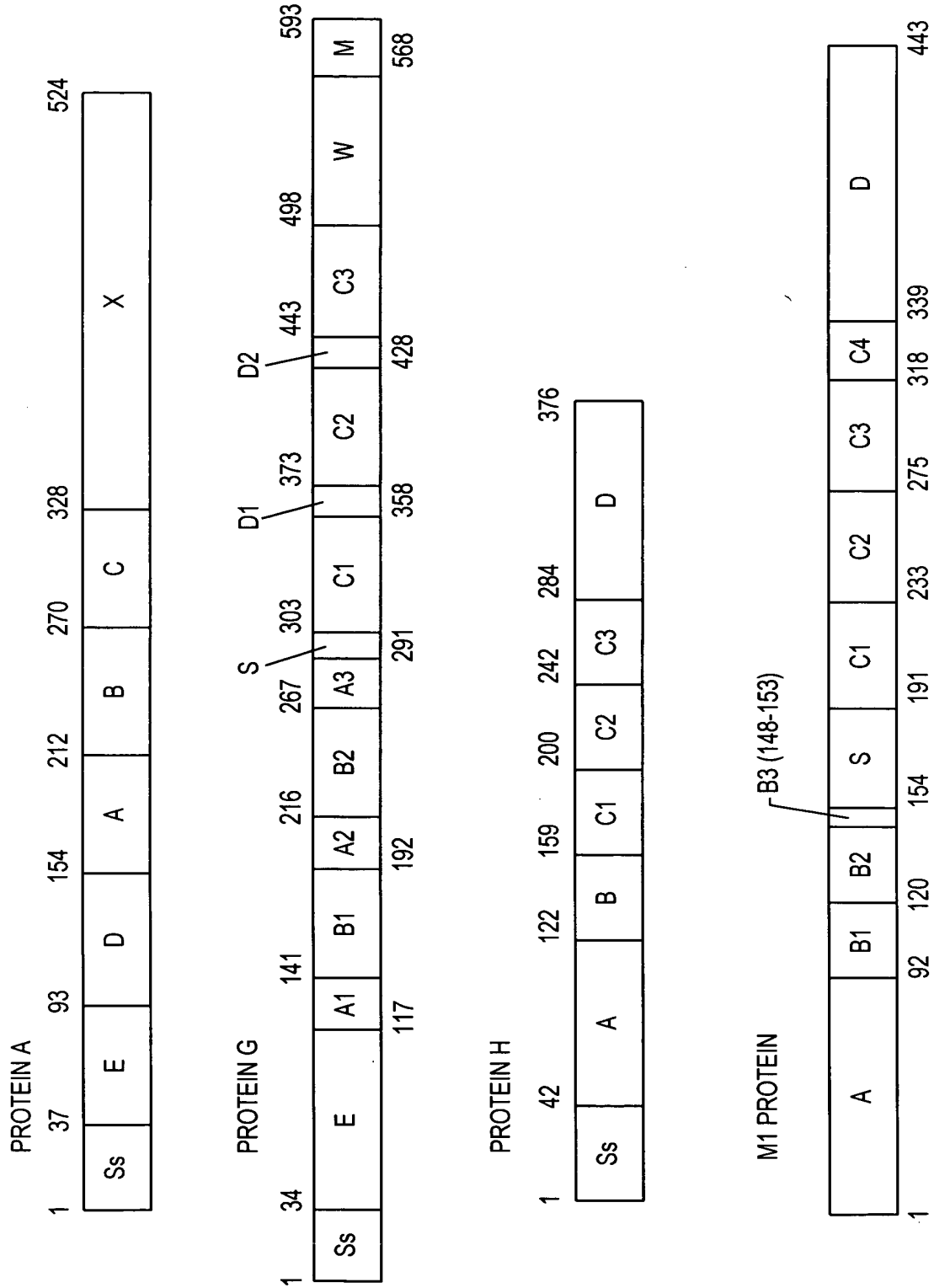
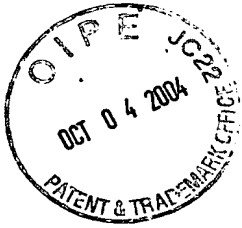
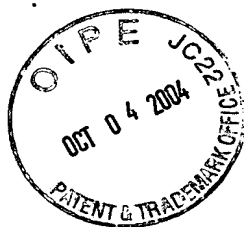


FIG. 5c





AACGGTGATGGTAAATCCTAGGGAAGTTATAGAAAGATCTTGCAGCAAAACAATCCCGCAATA 60
AsnGlyAsoGlyAsnProArgGluValIleGluAspLeuAlaAlaAsnAsnFroAlaIle 20

CAAAATATACGTTTACGTCACGAAACAAAGGACTTAAAGCGAGATTAGAGAATGCAATG 120
GlnAsnIleArgLeuArgHisGluAsnLysAspLeuLysAlaArgLeuGluAsnAlaMet 40

GAAGTTGCAGGAAGAGATTTTAAGAGAGCTGAAGAACTTGAAAAAGCAAAACAAGCCTTA 180
GluValAlaGlyArgAspPheLysArgAlaGluGluLeuGluLysAlaLysGlnAlaLeu 60

GAAGACCAGCGTAAAGATTTAGAAACTAAATTAAAGAACTACAACAAGACTATGACTTA 240
GluAspGlnArgLysAspLeuGluThrLysLeuLysGluLeuGlnGlnAspTyrAspLeu 80

GCAAAAGGAATCAACAAGTTGGGATAGACAAAGACTTGAAAAAGAGTTAGAAGAGAAAAAG 300
AlaLysGluSerThrSerTrpAspArgGlnArgLeuGluLysGluLeuGluGluLysLys 100

GAAGCTCTTGAATTAGCGATAGACCAGGCAAGTCGGGACTACCATAGAGCTACCGCTTTA 360
GluAlaLeuGluLeuAlaIleAspGlnAlaSerArgAspTyrHisArgAlaThrAlaLeu 120

GAAAAAGAGTTAGAAAGAAAAAGAAAGCTCTTGAATTAGCGATAGACCAAGCGAGTCAG 420
GluLysGluLeuGluGluLysLysAlaLeuGluLeuAlaIleAspGlnAlaSerGln 140

GACTATAATAGAGCTAACGTCTTAGAAAAAGAGTTAGAAAACGATTACTAGAGAAACAAGAG 480
AspTyrAsnArgAlaAsnValLeuGluLysGluLeuGluThrIleThrArgGluGlnGlu 160

ATTAATCGTAATCTTTTAGGCAATGCAAAAACCTTGAACTTGATCAACTTTCATCTGAAAAA 540
IleAsnArgAsnLeuLeuGlyAsnAlaLysLeuGluLeuAspGlnLeuSerSerGluLys 180

FIG.7a

[illegible]

AMINO ACID SEQUENCE AND NUCLEIC ACID SEQUENCE FOR PROTEIN M1, IgG-BINDING SOMEWHERE BETWEEN AMINO ACID 1-190.

FIG. 7b

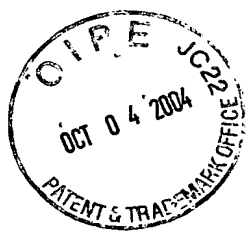


840
280
900
300
960
320
1020
340
1080
360
1140
380
1200
400
1260
420
1320
440

G A A A A G A T T T A G C A A A C T T G A C T G C T G A A C T T G A T A A G G T T A A G A G A A A A A C A A A T C
G l u L y s A s p L e u A l a A s n L e u T h r A l a G l u L e u A s p L y s V a l L y s G l u G l u L y s G l n I l e
T C A G A C G C A A G C C G T C A A C G G C T T C G C C G T G A C T T G G A C G C A T C A C G T G A A G C T A A G A A A
S e r A s p A l a S e r A r g L e u A r g A s p L e u A s p A l a S e r A r g G l u A l a L y s L y s
C A A G T T G A A A A G C T T T A G A A G A A G C A A A C A G C A A A T T A G C T G C T C T T G A A A A A C T T A A C
G l n V a l G l u L y s A l a L e u G l u A l a A s n S e r L y s L e u A l a A l a L e u G l u L y s L e u A s n
A A G A G C T T G A A G A A A G C A A G A A T T A A C A G A A A A A A A G C T G A A C T A C A A G C A A A A
L y s G l u L e u G l u S e r L y s L y s L e u T h r G l u L y s G l u L y s A l a G l u L e u G l n A l a L y s
C T T G A A G C A A G C A A A A G C A C T C A A G A A C A A T T A G C G A A A C A A G C T G A A G A A C T C G C A
L e u G l u A l a G l u A l a L y s A l a L e u L y s G l u G l n L e u A l a L y s G l n A l a G l u G l u L e u A l a
A A A C T A A G A G C T G G A A A A G C A T C A G A C T C A C A A A C C C C T G A T A C A A A A C C A G G A A A C A A A
L y s L e u A r g A l a G l y L y s A l a S e r A s p S e r G l n T h r P r o A s p T h r L y s P r o G l y A s n L y s
G C T G T T C C A G G T A A A G G T C A A G C A C C A C A A G C A G G T A C A A A A C C T A A C C A A A A C A A A G C A
A l a V a l P r o G l y L y s G l y G l n A l a P r o G l n A l a G l y T h r L y s P r o A s n G l n A s n L y s A l a
C C A A T G A A G G A A A C T A A G A G A C A G T T A C C A T C A A C A G G T G A A A C A G C T A A C C C A T T C T T C
P r o M e t L y s G l u T h r L y s A r g G l n L e u P r o S e r T h r G l y G l u T h r A l a A s n P r o P h e
A C A G C G G C A C G C G T T A C T G T T A T G G C A A C A G C T G G A G T A G C A G C A G T T G T A A A A C G C A A A
T h r A l a A l a A r g V a l T h r V a l M e t A l a T h r A l a G l y V a l A l a A l a V a l V a l L y s A r g L y s

G A A G A A A A C T A A 1329
G l u G l u A s n > > > 443

FIG.7c



17 / 18

PROBE:

IgG



PROTEIN LG
PROTEIN L
PROTEIN G

Ig kappa



PROTEIN LG
PROTEIN L
PROTEIN G

IgG Fc



PROTEIN LG
PROTEIN L
PROTEIN G

16 kDa —
35 kDa —
50 kDa —

FIG. 8

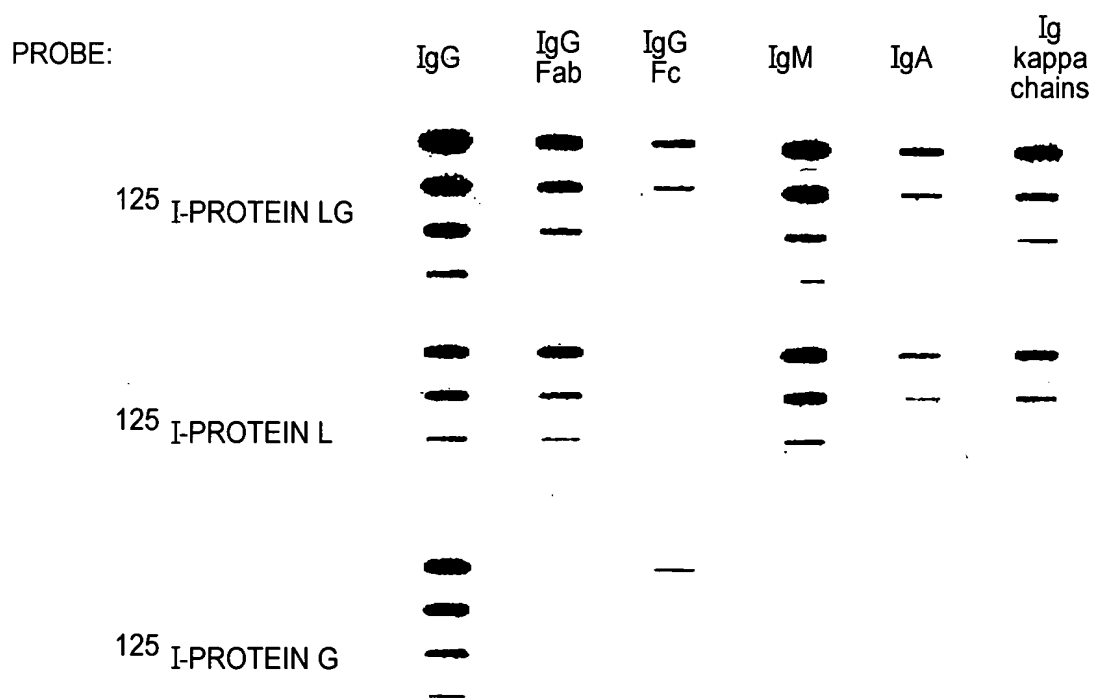
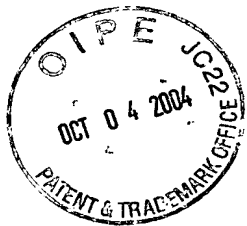


FIG. 9